Cortical layers imaging with inversion recovery MRI

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Introduction

Cyto-architecture and myelo-architecture are histological features that delineate the neuronal morphology of the tissue. More than one hundred years ago, Brodmann (1) and others observed this phenomenon and were able to identify six distinct layers of cellular arrangement in the cortex. Based on layers arrangement throughout the cortex, parcellation of cortex to neuro-anatomical regions was achieved. This segmentation is the basis of brain atlases used for neurosurgical navigation and brain mapping research. The identification of the cyto-architecture of the cortical layers relays on histological procedures therefore suffers from the its known limitations: the need to sacrifice the animal and work on post mortem tissue, the artifact of fixation and cutting (tissue disintegration, fracturing, and shrinkage). Currently there is no in-vivo imaging modality that enables accurate and robust visualization of neuronal cell structures mainly due to resolution limitations as the width of the cortex is about 2-4mm and the layers ranging from 0.2-1mm. Magnetic resonance imaging (MRI) is the non-invasive, in-vivo imaging modality that provides the best anatomical details on the human brain. Recently we developed a novel MRI acquisition and analysis framework (virtual definition of neuronal tissue by cluster analysis of multi-parametric MRI, virtual-dot-com (2)) that enables characterization and segmentation of cortical and sub-cortical structures with high resemblance to their cyto-architectonic mapping. In this work we applied this framework on multi-dimensional inversion recovery data set of the human and rat brains in order to segment the cortex into laminar arrangement.

Materials and methods

Rat Experiments: Two Wistar male rats (11 months) underwent MRI in a 7T scanner (Bruker). The protocol included 7 inversion recovery RARE acquisitions with the following parameters: TR/TE=4500/24ms, matrix of 192x160 (reconstructed to 256x256) with final pixel size of 0.125x0.125mm^2 and slice thickness of 1mm (five slices in coronal plane). The inversion time varied for each experiment at the following values: 730, 820, 860, 920, 990, and 1080ms. Following the MRI the rat brain were excised and prepared for cyto-architectonic histological analysis (Nissl stain).

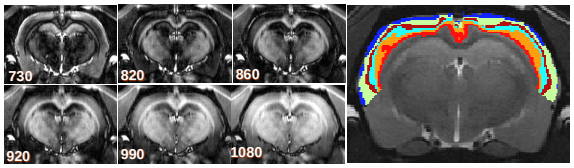

Figure 1: multi-spectral inversion recovery data set of the rat brain along with its clustering pattern.

Human Experiments: Six subjects (aged 25-35) underwent MRI in a 3T scanner (GE). The protocol included 7 inversion recovery sequences with the following parameters: TR/TE=10000/8.4ms, matrix of 512x384 (reconstructed to 512x512) with final pixel size of 0.39x0.39mm^2 and slice thickness of 3mm covering the entire brain (42 slices in axial plane). The inversion time varied for each experiment at the following values: 230, 432, 575, 760, 920, 1080, 1380, 2100ms. In addition conventional T1-SPGR was collected at similar resolution. The total MRI protocol lasted for 40 minutes.

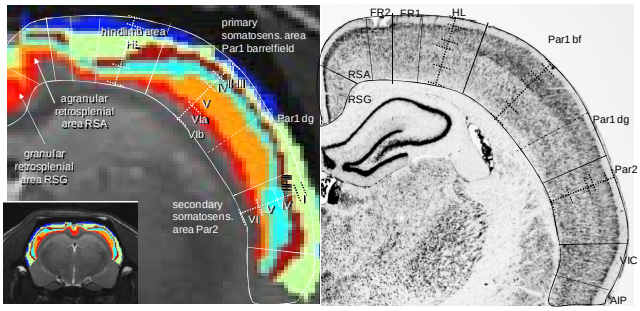

Figure 2: MRI cortical clusters compared with cyto-architectonic analysis

Image Analysis: The images were analyzed according to the virtual-dot-com framework (2). Briefly, following the co-registration (to correct for head movements), the cortex was automatically segmented, on which we used basic contrast enhancement in order to exclude outlier pixels thus stretching the dynamic range of the image. Next we performed cluster analysis based on the multi-parametric data including the following steps: 1. Normalizing the data to create a uniform scale between the different imaging methods. 2. Transforming the data into its P.C.A (principle component analysis) space to increase the variance. 3. Running a clustering algorithm such as "K-means".

Results and Discussion

Figure 1 depicts a multi-spectral inversion recovery (the inversion time are indicated on the images) data set of the rat brain along with the virtual-dot-com clusters of same data set. From the clustered image it is evident that the cortex can be segmented into a laminar pattern of layers. The inversion time were selected to zero the signal from different portions of the cortex at each experiment thus enabling the separation between layers. Figure 2 shows comparison of the MRI layers with cyto-architectonic analysis. It appears that the MRI layers do not follow the cyto-architectonic segmentation in all regions but there is good agreement between them. It appears that the border between layers I and II is not well defined in MRI segmentation. Similar data set but on the human brain is shown in Figure 3, with sufficient resolution it is possible to see the progression of the IR zero signal band along the cortex at the different inversion time images. Cluster analysis of the data also reveals and enables quantification of the laminar segmentation of the cortex from the inversion recovery images.

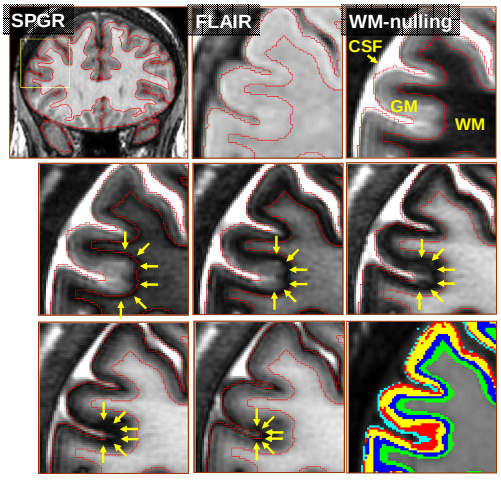

Figure 3: multi-spectral inversion recovery data set of the human brain along with its clustering pattern.

Conclusion

Multi spectral inversion recovery imaging enable characterization of the laminar segmentation of the cortex. By zeroing the signal of each layer and producing the multi-spectral data set, tissue classification algorithms (such as the virtual-dot-com framework) enable visualization and quantification of the observed layers. The MRI layers seem to be in good agreement with the cyto-architectonic segmentation. Further optimization of the acquisition and analysis protocol may provide a framework for subject specific cortical layer imaging.

References:

1. Brodmann K, Garey L. Brodmann's Localisation in the cerebral cortex. London River Edge, NJ: Imperial College Press ; 2. Yovel Y, Assaf Y. Virtual definition of neuronal tissue by cluster analysis of multi-parametric imaging (virtual-dot-com imaging). Neuroimage 2007;35(1):58-69.